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OM nucleic - nucleic search, using sw model

Run on: November 5, 2004, 19:26:33 ; Search time 87 Seconds  
(without alignments)  
4027.804 Million cell updates/sec

Title: US-09-882-434A-2  
Perfect score: 493  
Sequence: 1 attaatgtcttgatgtctcat.....ccatgtgatgttttacc 493

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 35539441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

- Database :
- 1: /cgn2\_6/ptodata/1/ina/5A\_COMB.seq.\*
  - 2: /cgn2\_6/ptodata/1/ina/5B\_COMB.seq.\*
  - 3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq.\*
  - 4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq.\*
  - 5: /cgn2\_6/ptodata/1/ina/PCUTS\_COMB.seq.\*
  - 6: /cgn2\_6/ptodata/1/ina/backfiles.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
C 1	34.8	7.1	179	US-09-382-552-43	Sequence 43, Appl
C 2	34	6.9	337	US-09-270-767-29138	Sequence 29138, A
C 3	34	6.9	1133	US-09-270-767-13217	Sequence 13217, A
C 4	33.4	6.8	9223	US-08-961-527-59	Sequence 59, Appl
C 5	33	6.7	62909	US-09-596-002-32	Sequence 32, Appl
C 6	32.4	6.6	972	US-09-248-796A-13663	Sequence 13663, A
C 7	32.2	6.5	1137	US-09-248-796A-4423	Sequence 4423, Ap
C 8	32.2	6.5	1422	US-09-134-001C-1936	Sequence 1936, Ap
C 9	32	6.5	291	US-09-540-236-398	Sequence 398, Ap
C 10	32	6.5	92407	US-09-596-002-36	Sequence 36, Appl
C 11	32	6.5	202001	US-09-734-674-3	Sequence 3, Appl
C 12	31.8	6.5	537	US-08-845-539-5	Sequence 5, Appl
C 13	31.8	6.5	537	US-09-362-642-5	Sequence 5, Appl
C 14	31.6	6.4	6354	US-09-058-389A-5	Sequence 5, Appl
C 15	31.6	6.4	6354	US-09-611-781-5	Sequence 5, Appl
C 16	31.6	6.4	1664976	US-08-916-421B-1	Sequence 1, Appl
C 17	31.6	6.4	1664976	US-09-692-570-1	Sequence 1, Appl
C 18	31.4	6.4	561	US-09-540-236-1317	Sequence 1317, Ap
C 19	31.4	6.4	3189	US-09-710-279-3694	Sequence 3694, Ap
C 20	31.4	6.4	3223	US-09-710-279-4222	Sequence 4222, Ap
C 21	31.4	6.4	246240	US-08-724-394A-20	Sequence 20, Appl
C 22	31.4	6.4	246240	US-08-724-394A-21	Sequence 21, Appl
C 23	31.4	6.4	246240	US-08-724-394A-22	Sequence 22, Appl
C 24	31.4	6.4	1664976	US-08-916-421B-1	Sequence 1, Appl
C 25	31.4	6.4	1664976	US-09-692-570-1	Sequence 1, Appl
C 26	31.2	6.3	4417	US-07-741-453A-57	Sequence 57, Appl
C 27	31.2	6.3	5915	US-09-382-552-3	Sequence 3, Appl

C 28	31.2	6.3	6240	4	US-09-382-552-117	Sequence 117, Appl
C 29	31.2	6.3	6909	4	US-09-382-552-21	Sequence 21, Appl
C 30	31.2	6.3	6910	4	US-09-382-552-15	Sequence 15, Appl
C 31	31.2	6.3	6911	4	US-09-382-552-1	Sequence 1, Appl
C 32	31.2	6.3	6911	4	US-09-382-552-14	Sequence 14, Appl
C 33	31.2	6.3	6911	4	US-09-382-552-16	Sequence 16, Appl
C 34	31.2	6.3	6911	4	US-09-382-552-17	Sequence 17, Appl
C 35	31.2	6.3	6911	4	US-09-382-552-18	Sequence 18, Appl
C 36	31.2	6.3	6911	4	US-09-382-552-19	Sequence 19, Appl
C 37	31.2	6.3	6911	4	US-09-382-552-20	Sequence 20, Appl
C 38	31.2	6.3	6912	4	US-09-382-552-13	Sequence 13, Appl
C 39	31	6.3	4301	3	US-08-121-446-3	Sequence 3, Appl
C 40	31	6.3	112132	4	US-09-741-150-3	Sequence 3, Appl
C 41	31	6.3	112132	4	US-10-160-187-3	Sequence 3, Appl
C 42	30.8	6.2	444	4	US-09-248-796A-3435	Sequence 3435, Ap
C 43	30.8	6.2	3715	3	US-09-600-776-9	Sequence 9, Appl
C 44	30.6	6.2	1569	4	US-09-248-796A-2847	Sequence 2847, Ap
C 45	30.6	6.2	5361	3	US-08-973-462-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1

US-09-382-552-43/c  
; Sequence 43, Application US/09382552  
; Patent No. 6673909  
; GENERAL INFORMATION:  
; APPLICANT: Brown, Jr., Robert H.  
; APPLICANT: Liu, Jing  
; APPLICANT: Aoki, Masashi  
; APPLICANT: Ho, Meng  
; APPLICANT: Matsuda-Asada, Chie  
; TITLE OF INVENTION: DYSPERLIN, A GENE MUTATED IN DISTAL MYOPATHY AND LIMB GIRDLE MUSCULAR DYSTROPHY  
; FILE REFERENCE: 00786/399002  
; CURRENT APPLICATION NUMBER: US/09/382,552  
; CURRENT FILING DATE: 1999-08-25  
; EARLIER APPLICATION NUMBER: US 60/097,927  
; EARLIER FILING DATE: 1998-08-25  
; NUMBER OF SEQ ID NOS: 233  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 43  
; LENGTH: 179  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-382-552-43

Query Match 7.1%; Score 34.8; DB 4; Length 179;  
Best Local Similarity 65.4%; Pred. No. 0.11;  
Matches 51; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY	22	CATACCTCTTCCTCCCAACCATAGCACTTATCAGTAACTCAGCTAGCCATGCGCTTCCACC	81
Db	155	CTGCTCCTCTGCTCTTACCATTTCCCGCAAGCTGACCTCCACAAAGGGTCCACC	96
QY	82	AGTTGTTCTTCTCAGTC	99
Db	95	AAGTTCTTCTTGTACTC	78

RESULT 2

US-09-270-767-29138  
; Sequence 29138, Application US/09270767  
; Patent No. 6703491  
; GENERAL INFORMATION:  
; APPLICANT: Homburger et al.  
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster  
; FILE REFERENCE: File Reference: 7328-094  
; CURRENT APPLICATION NUMBER: US/09/270,767  
; CURRENT FILING DATE: 1999-03-17  
; NUMBER OF SEQ ID NOS: 62517  
; SOFTWARE: PatentIn Ver. 2.0

```
; SEQ ID NO 29138
; LENGTH: 337
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-29138

Query Match
Best Local Similarity 6.9%; Score 34; DB 4; Length 337;
Matches 82; Conservative 0; Mismatches 80; Indels 0; Gaps 0;

QY 329 CCAGGCGCATGCAACCCCTTTGGTTGGAGAGATATCTTCATCCAAATGCTAGATTTTCATAAC 388
Db 13 CAAGGGCGCACCTCCGCTTTTGGTTGGTTATCAATGCTAGCCATTGAATATATATAT 72

QY 389 TCTTGGATCCATCTTCTATGTTTTCAGTGTATATTAATAGAGAGATGCTGATATATAA 448
Db 73 ATTATCAATTTTCATTACATTAATCACTTATATTAATCAACATATGATTAATGAAATTGG 132

QY 449 TAAATAAGTAAAGCTACGGTATCACCATGTCATGATTTTAA 490
Db 133 TACAGTCTGAAATATGCGTTTATACGAACGATATTTTAA 174

RESULT 3
US-09-270-767-13217
; Sequence 13217, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 13217
; LENGTH: 1137
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-13217

Query Match
Best Local Similarity 6.9%; Score 34; DB 4; Length 1133;
Matches 82; Conservative 0; Mismatches 80; Indels 0; Gaps 0;

QY 329 CCAGGCGCATGCAACCCCTTTGGTTGGAGAGATATCTTCATCCAAATGCTAGATTTTCATAAC 388
Db 13 CAAGGGCGCACCTCCGCTTTTGGTTGGTTATCAATGCTAGCCATTGAATATATATATAT 72

QY 389 TCTTGGATCCATCTTCTATGTTTTCAGTGTATATTAATAGAGAGATGCTGATATATAA 448
Db 73 ATTATCAATTTTCATTACATTAATCACTTATATTAATCAACATATGATTAATGAAATTGG 132

QY 449 TAAATAAGTAAAGCTACGGTATCACCATGTCATGATTTTAA 490
Db 133 TACAGTCTGAAATATGCGTTTATACGAACGATATTTTAA 174

RESULT 4
US-08-961-527-59/c
; Sequence 59, Application US/08961527
; Patent No. 6420135
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 351
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,527
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB340P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
LENGTH: 9223 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-961-527-59

Query Match
Best Local Similarity 6.8%; Score 33.4; DB 4; Length 9223;
Matches 70; Conservative 1; Mismatches 62; Indels 0; Gaps 0;

QY 360 TATCTTTCATCCAAATGCTAGATTTTCATAACTCTTGATCCATCTTCTATGTTTTCAGTG 419
Db 4971 TATTTTCAAAAATATATCATATAGTTCATCTTCAGTAATTTTCTATATTTTCGTTGCAG 4912

QY 420 TATAATTAGAGATGCTGATATATAATAAAGTAAAGCTACGGTATCACCATCT 479
Db 4911 TCCAAATGAAATAGCTTGTAATCATAAGAAACAGGTGATGCAATGAATTAAGTCT 4852

QY 480 GATGATTTTACC 492
Db 4851 TGTGAAAGCTACC 4839

RESULT 5
US-09-596-002-32/c
; Sequence 32, Application US/09596002
; Patent No. 6632636
; GENERAL INFORMATION:
; APPLICANT: Lagace, Robert, E.
; APPLICANT: Patterson, Chandra
; APPLICANT: Berg, Kim, L.
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF MORAXELLA CATARRHALIS GENOME
; FILE REFERENCE: PM-0008-4 US
; CURRENT APPLICATION NUMBER: US/09/596,002
; CURRENT FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: 60/140,121
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PERL Program
; SEQ ID NO 32
; LENGTH: 62909
; TYPE: DNA
; ORGANISM: M. catarrhalis
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte template ID No. 6632636 32
; PUBLICATION INFORMATION:
US-09-596-002-32

Query Match
Best Local Similarity 6.7%; Score 33; DB 4; Length 62909;
Matches 69; Conservative 0; Mismatches 60; Indels 0; Gaps 0;
```

US-09-248-796A-4423

Query Match 6.5%; Score 32.2; DB 4; Length 1137;  
Best Local Similarity 56.0%; Pred. No. 2.3;  
Matches 61; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

QY 327 TGCAGGCGATCAACCCCTTTGGTTGGAGAGATATCTTCATCCAAATGCTAGATTTTCAAT 386  
Db 57540 TGCACAGAAATCGAGCTTACGGGTTCATCTATGCTTCGCCAATGCTGATTTGAT 57481

QY 387 ACTCTTGGATCCATCTTCTATGTTTTCAGTGTATATAATTAGAGAGATGCATGATATAT 446  
Db 57480 AATTTTGCATAAATCTGTAGATTGCTCTTGGCTGAGTGCATGAACCTTGGTTGGATATTT 57421

QY 447 AATAATAAA 455  
Db 57420 GATCCAAAA 57412

RESULT 6  
US-09-248-796A-13663/c  
; Sequence 13663, Application US/09248796A  
; Patent No. 6747137  
; GENERAL INFORMATION:  
; APPLICANT: Keith Weinstock et al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN  
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 107196.132  
; CURRENT APPLICATION NUMBER: US/09/248,796A  
; CURRENT FILING DATE: 1999-02-12  
; PRIOR APPLICATION NUMBER: US 60/074,725  
; PRIOR FILING DATE: 1998-02-13  
; PRIOR APPLICATION NUMBER: US 60/096,409  
; PRIOR FILING DATE: 1998-08-13  
; NUMBER OF SEQ ID NOS: 28208  
; SEQ ID NO 13663  
; LENGTH: 972  
; TYPE: DNA  
; ORGANISM: Candida albicans  
US-09-248-796A-13663

Query Match 6.6%; Score 32.4; DB 4; Length 972;  
Best Local Similarity 48.9%; Pred. No. 1.8;  
Matches 87; Conservative 0; Mismatches 91; Indels 0; Gaps 0;

QY 288 TGGATGCGAGTGTGTGACACACAGAGTTTGGGTCCAGTGCCAGGGGATGCAACCCCTTT 347  
Db 751 TTGATTCAGTGTGTGACAAACACAGATGTAATGTTTGTGTTAATCCAGACATT 692

QY 348 TGGTGGAGAGATCTTCATCCATGCTAGATTTCAATCTTTGGATCCATCTTCAT 407  
Db 691 TACCAGTACGAGTGGATTCACCAATGAATAAGTAGACACACTGATAGTCCAGTAAT 632

QY 408 GTTTTCAAGTGTATAATTAGAGAGATGATGATATATAATAAATAAGTAAAGCTA 465  
Db 631 TTGATTCATAGTTGGAATTGATTGTTGACTAGATTCAGCTTTTAAAGATGAACATA 574

RESULT 7  
US-09-248-796A-4423/c  
; Sequence 4423, Application US/09248796A  
; Patent No. 6747137  
; GENERAL INFORMATION:  
; APPLICANT: Keith Weinstock et al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN  
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 107196.132  
; CURRENT APPLICATION NUMBER: US/09/248,796A  
; CURRENT FILING DATE: 1999-02-12  
; PRIOR APPLICATION NUMBER: US 60/074,725  
; PRIOR FILING DATE: 1998-02-13  
; PRIOR APPLICATION NUMBER: US 60/096,409  
; PRIOR FILING DATE: 1998-08-13  
; NUMBER OF SEQ ID NOS: 28208  
; SEQ ID NO 4423  
; LENGTH: 1137  
; TYPE: DNA  
; ORGANISM: Candida albicans

US-09-134-001C-1936/c

Query Match 6.5%; Score 32.2; DB 3; Length 1422;  
Best Local Similarity 57.4%; Pred. No. 2.6;  
Matches 58; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

QY 371 AATGCTAGATTTTCATACCTTTGGATCCATCTTCTATCTTTTCAAGTGTATAATTAGAG 430  
Db 1232 AATCTCTCTTTGTTTAACTTCTCAATATATTGTGGAGATTAAATCAATTAATTTCTTT 1173

QY 431 AGATGCGATGATATATAATAAATAAGTAAAGCTAACGGTAT 471  
Db 1172 AGATACAATAATAATAATAAAGTAAAGCTCTGTCT 1132

RESULT 8  
US-09-134-001C-1936/c  
; Sequence 1936, Application US/09134001C  
; Patent No. 6380370  
; GENERAL INFORMATION:  
; APPLICANT: Lynn Doucette-Stamm et al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS  
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: GTC-007  
; CURRENT APPLICATION NUMBER: US/09/134,001C  
; CURRENT FILING DATE: 1998-08-13  
; PRIOR APPLICATION NUMBER: US 60/064,964  
; PRIOR FILING DATE: 1997-11-08  
; PRIOR APPLICATION NUMBER: US 60/055,779  
; PRIOR FILING DATE: 1997-08-14  
; NUMBER OF SEQ ID NOS: 5674  
; SEQ ID NO 1936  
; LENGTH: 1422  
; TYPE: DNA  
; ORGANISM: Staphylococcus epidermidis  
US-09-134-001C-1936

Query Match 6.5%; Score 32.2; DB 3; Length 1422;  
Best Local Similarity 57.4%; Pred. No. 2.6;  
Matches 58; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

QY 371 AATGCTAGATTTTCATACCTTTGGATCCATCTTCTATCTTTTCAAGTGTATAATTAGAG 430  
Db 1232 AATCTCTCTTTGTTTAACTTCTCAATATATTGTGGAGATTAAATCAATTAATTTCTTT 1173

QY 431 AGATGCGATGATATATAATAAATAAGTAAAGCTAACGGTAT 471  
Db 1172 AGATACAATAATAATAATAAAGTAAAGCTCTGTCT 1132

RESULT 9  
US-09-540-236-398/c  
; Sequence 398, Application US/09540236  
; Patent No. 6673910  
; GENERAL INFORMATION:  
; APPLICANT: Gary L. Breton et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATRA  
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 2709.2005-001  
; CURRENT APPLICATION NUMBER: US/09/540,236  
; CURRENT FILING DATE: 2000-04-04  
; NUMBER OF SEQ ID NOS: 3840  
; SEQ ID NO 398  
; LENGTH: 291  
; TYPE: DNA  
; ORGANISM: M. catarrhalis  
US-09-540-236-398

Query Match 6.5%; Score 32; DB 4; Length 291;  
Best Local Similarity 54.2%; Pred. No. 1.2;  
Matches 65; Conservative 0; Mismatches 55; Indels 0; Gaps 0;

QY 363 CTTCATCCAAATGCTAGATTTCATACTCTTGGATCCATCTTCTATGTTTTCAGGTAT 422

Db 159 CTCAGCCATCTCTGTTTTTATACAAACACGCACTTCAAGTTTTTGATCGCAGT 100  
QY 423 AATTAGAGATGCGATGATATATAAATAAGTAAAGCTACCGTATCACCATGTGAT 482  
Db 99 TTTTGTGTGAAATTTTGTATTATATCAAAACATTTAAGGCAAGGTATGCCCATATGAT 40

## RESULT 10

US-09-596-002-36/c  
; Sequence 36, Application US/09596002  
; Patent No. 6632636  
; GENERAL INFORMATION:

; APPLICANT: Lagace, Robert, E.

; APPLICANT: Patterson, Chandra

; APPLICANT: Berg, Kim, L.

; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF MORAXELLA CATARRHALIS GENOME

; FILE REFERENCE: PM-0008-4 US

; CURRENT APPLICATION NUMBER: US/09/596,002

; CURRENT FILING DATE: 2000-06-16

; PRIOR APPLICATION NUMBER: 60/140,121

; PRIOR FILING DATE: 1999-06-18

; NUMBER OF SEQ ID NOS: 41

; SOFTWARE: PERL Program

; SEQ ID NO 36

; LENGTH: 92407

; TYPE: DNA

; ORGANISM: M. catarrhalis

; NAME/KEY: misc feature

; OTHER INFORMATION: Incyte template ID No. 6632636 36

; PUBLICATION INFORMATION:

US-09-596-002-36

## Query Match

Best Local Similarity 6.5%; Score 32; DB 4; Length 92407;

Mismatches 65; Conservative 0; Mismatches 55; Indels 0; Gaps 0;

QY 363 CTCATCAAGCTAGATTTCATTAATCTTGGATCCATCTTCTATGTTTTCAGTGTAT 422  
Db 66073 CTCAGCCATCTCTGTTTTTATACAAACGCACTTCAAGTTTTTGATCGCAGT 66014  
QY 423 AATTAGAGATGCGATGATATATAAATAAGTAAAGCTACCGTATCACCATGTGAT 482  
Db 66013 TTTTGTGTGAAATTTTGTATTATATCAAAACATTTAAGGCAAGGTATGCCCATATGAT 65954

## RESULT 11

US-09-734-674-3/c

; Sequence 3, Application US/09734674

; Patent No. 6498022

; GENERAL INFORMATION:

; APPLICANT: WEI, Ming-Hui et al

; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,

; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,

; TITLE OF INVENTION: AND USES THEREOF

; FILE REFERENCE: CL001018

; CURRENT APPLICATION NUMBER: US/09/734,674

; CURRENT FILING DATE: 2000-12-13

; NUMBER OF SEQ ID NOS: 4

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 3

; LENGTH: 202001

; TYPE: DNA

; ORGANISM: Human

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (1)...(202001)

; OTHER INFORMATION: n = A,T,C or G

US-09-734-674-3

## Query Match

Best Local Similarity 6.5%; Score 32; DB 4; Length 202001;

Mismatches 56; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

Matches 59; Conservative 0; Mismatches 45; Indels 0; Gaps 0;  
QY 10 TTGAGTCTCATACATCTCTTCTCTCCCAACATTAGCACTTATCAGCTAACCTCAGCC 69  
Db 150243 TTGAGTTGAATACTGATTCTGCCCTTTCTAGCTATTGATCTTAGCAATCACCACCC 150184  
QY 70 ATGGCTTCCACCAAGTTGTTCTTCTCAGTCATCTACTGTGATCAT 113  
Db 150183 CTGAGTTTCTATGAATTCATTATATAACTAATAATAATAATTAT 150140

## RESULT 12

US-08-845-539-5

; Sequence 5, Application US/08845539

; Patent No. 5929303

; GENERAL INFORMATION:

; APPLICANT: Bennett, Alan B.

; APPLICANT: Rose, Jocelyn K.C.

; TITLE OF INVENTION: Fruit-Specific and Ripening-Regulation

; TITLE OF INVENTION: Expansin Genes to Control Fruit Texture and Softening

; NUMBER OF SEQUENCES: 8

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend and Crew LLP

; STREET: Two Embarcadero Center, Eighth Floor

; CITY: San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94111-3834

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/845,539

; FILING DATE: 25-APR-1997

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Bastian, Kevin L.

; REGISTRATION NUMBER: 34,774

; REFERENCE/DOCKET NUMBER: 023070-0782000US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 576-0200

; TELEFAX: (415) 576-0300

; INFORMATION FOR SEQ ID NO: 5:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 537 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 1..537

; OTHER INFORMATION: /product= "melon CmEx1"

US-08-845-539-5

## Query Match

Best Local Similarity 6.5%; Score 31.8; DB 2; Length 537;

Mismatches 69; Conservative 0; Mismatches 62; Indels 0; Gaps 0;

QY 238 GGCTATGACTTCAGTACACTGGACAACTGCTCTCTCTACACCGGCTGGATGCAGT 297  
Db 82 GGCTATGGCGTCAACACAGCTGCTCTTAGTACTGTTTCTTCAACAATGGCGCTAGCTGT 141  
QY 298 GGTCTTGCACACACAGGTTTGGGTCCAGTCCAGGGGATCAACCCCTTTTGGTTGGAAG 357  
Db 142 GGTGCTTGTGATCAAGTGTGCTAATGACCTCGATGCTGCTATGCTTGGTAGCCCT 201  
QY 358 AGTATCTTCAT 368  
Db 202 TGTATCTTCAT 212

RESULT 13  
US-09-362-642-5  
; Sequence 5, Application US/09362642  
; Patent No. 6350935  
; GENERAL INFORMATION:  
; APPLICANT: Bennett, Alan B.  
; APPLICANT: Rose, Jocelyn K.C.  
; APPLICANT: The Regents of the University of California  
; TITLE OF INVENTION: Fruit-Specific and Ripening Regulation Expansin Genes  
; TITLE OF INVENTION: to Control Fruit Texture and Softening  
; FILE REFERENCE: 023070-078210US  
; CURRENT APPLICATION NUMBER: US/09/362,642  
; CURRENT FILING DATE: 1999-07-27  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 5  
; LENGTH: 537  
; TYPE: DNA  
; ORGANISM: Cucumis melo  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(537)  
; OTHER INFORMATION: melon expansin (CmEx1) partial cDNA clone  
; US-09-362-642-5  
  
Query Match 6.5%; Score 31.8; DB 3; Length 537;  
Best Local Similarity 52.7%; Pred. No. 2;  
Matches 69; Conservative 0; Mismatches 62; Indels 0; Gaps 0;  
  
Qy 238 GGCTATGACTTCACTACACTGCGCAAACTGCTCTCTCAACACCGCTGGATGAGT 297  
Db 82 GGCTATGGGTCACACAGCTGCTTTAGTACTGCTTTCTTCAACAATGGCCTCAGCTGT 141  
Qy 298 GGTTGTCACACACACAGCTTTGGTCCAGTCGCCAGGCGATCAACCTTTTGGTGAAG 357  
Db 142 GGTGCTTGTGTTGAGATCAAGTGTCTTAATGACCTCGATGCTGCTGCTGGTGGCCT 201  
Qy 358 AGTATCTTCAT 368  
Db 202 TGTATCTTCAT 212  
  
RESULT 14  
US-09-058-389A-5  
; Sequence 5, Application US/09058389A  
; Patent No. 6130065  
; GENERAL INFORMATION:  
; APPLICANT: Belt, Judith A.  
; APPLICANT: Crawford, Charles R.  
; APPLICANT: Patel, Divyen  
; TITLE OF INVENTION: A NITROBENZYLMECAPTOPURINERIBOSIDE  
; TITLE OF INVENTION: (NEMPR)-INSENSITIVE, EQUILIBRATIVE, NUCLEOSIDE TRANSPORT  
; TITLE OF INVENTION: PROTEIN, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF  
; TITLE OF INVENTION: USE  
; NUMBER OF SEQUENCES: 22  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: David A. Jackson, Esq.  
; STREET: 411 Hackensack Ave, Continental Plaza, 4th  
; CITY: Hackensack  
; STATE: New Jersey  
; COUNTRY: USA  
; ZIP: 07601  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/058,389A  
; FILING DATE: April 9, 1998  
; CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:  
; NAME: Jackson Esq., David A.  
; REGISTRATION NUMBER: 26,742  
; REFERENCE/DOCKET NUMBER: 1340-1-013N  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 201-487-5800  
; TELEFAX: 201-343-1684  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 6354 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; HYPOTHETICAL: NO  
; US-09-058-389A-5  
  
Query Match 6.4%; Score 31.6; DB 3; Length 6354;  
Best Local Similarity 46.4%; Pred. No. 9.4;  
Matches 103; Conservative 0; Mismatches 119; Indels 0; Gaps 0;  
  
Qy 78 CACCAAGTTCTTCTCAGTCATTACTGTGATGATGCTCATAGCAATGGCAAGTGAGAT 137  
Db 5639 CACCTCTCGTCTTCTCCCGCCATCACAGCCATGGTGACCAAGTCTCCACCAAGTCTGGAA 5698  
Qy 138 GGTGAATGGGAGTGCATTACAGTATGGAGTGTCCAGGTGTGAACACCGTGTCTGAGCG 197  
Db 5699 GTGAGTGTGAGTGTGAGGAGAGACGGCAGGGCAGGGGTACAAAGGGGAGGACG 5758  
Qy 198 ATATAGCAAGTGTGATGCTCAGCTATACATACAGAGGGAGGCTATGACTTCACTACAC 257  
Db 5759 GGACAGGGGAGTGGACACAGATGAGCTGCAGCCGTTTCCCTCCCAAGGTCACTTCTTC 5818  
Qy 258 TGGACAAACTGCTCTCTCTACAAACAGGCTGGATGAGTGG 299  
Db 5819 AACCCTATCTGCTGCTTCTCTCTTCAACATCATGAGCTGG 5860  
  
RESULT 15  
US-09-611-781-5  
; Sequence 5, Application US/09611781  
; Patent No. 6423829  
; GENERAL INFORMATION:  
; APPLICANT: Belt, Judith A.  
; APPLICANT: Crawford, Charles R.  
; APPLICANT: Patel, Divyen  
; TITLE OF INVENTION: A NITROBENZYLMECAPTOPURINERIBOSIDE  
; TITLE OF INVENTION: (NEMPR)-INSENSITIVE, EQUILIBRATIVE, NUCLEOSIDE TRANSPORT  
; TITLE OF INVENTION: PROTEIN, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF  
; TITLE OF INVENTION: USE  
; NUMBER OF SEQUENCES: 22  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: David A. Jackson, Esq.  
; STREET: 411 Hackensack Ave, Continental Plaza, 4th  
; CITY: Hackensack  
; STATE: New Jersey  
; COUNTRY: USA  
; ZIP: 07601  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/611,781  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 09/058,389  
; FILING DATE: April 9, 1998  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Jackson Esq., David A.

REGISTRATION NUMBER: 26,742  
REFERENCE/DOCKET NUMBER: 1340-1-013N  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201-487-5800  
TELEFAX: 201-343-1684  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6354 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
US-09-611-781-5

Query Match	6.4%;	Score 31.6;	DB 4;	Length 6354;
Best Local Similarity	46.4%;	Pred. No. 9.4;		
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QY	138	GGTGAATGGAGTGCATTTTACATATGGAGTGTGTCCAGTTGTATACAAACGTCCTGAGCG	197	
Db	5699	GTGGAGTGAAGTGTCAAGGTGGAAGAAGCGGAGGGGGGTACAAAGGGGAGAGGACG	5758	
QY	198	ATATAGCAAGTGTGGATGTCACGCTATACATCAAGAGGGAGGCTATCACTTCAGCTACAC	257	
Db	5759	GGAGAGGGAGTTGGAGACCAAGTATGAGCTGCAGCCGTTTCCCTCCAGGTGAGTTCTTC	5818	
QY	258	TGGACAAATGCTGCTCTCTTACAAACGAGCTGGATGACGTGG	299	
Db	5819	AAACCCATCTGCTGCTTCCTCTCTTCAACATCATGCACTGG	5860	

Search completed: November 5, 2004, 20:42:49  
Job time : 92 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: November 5, 2004, 20:38:03 ; Search time 376 Seconds  
(without alignments)

7059.492 Million cell updates/sec

Title: US-09-882-434A-2

Perfect score: 493

Sequence: 1 attaatgtttgagttcat.....ccatgtgatgttttacc 493

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3611042 seqs, 2692057975 residues

Total number of hits satisfying chosen parameters: 7222084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:\*

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2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq.*
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9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq.*
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11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq.*
12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
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15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq.*
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17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq.*
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19: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
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21: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	492.6	99.9	493	9	US-09-882-434A-2
2	39.6	8.0	632	18	US-10-425-115-66398
3	35.6	7.2	516	13	US-10-027-632-272863
4	35.6	7.2	516	15	US-10-027-632-272863
5	35.6	7.2	8011	15	US-10-311-455-51
6	35.4	7.2	2035	15	US-10-172-118-1814
7	35.4	7.2	2035	16	US-10-342-887-1814
8	35.4	7.2	2658	14	US-10-198-846-10674
9	35.4	7.2	3043	15	US-10-104-047-374
10	35.2	7.1	6375	15	US-10-311-455-1997
11	35.2	7.1	39342	16	US-10-221-714A-471
12	34.8	7.1	179	10	US-09-382-860-43
Sequence 2, Appli					
Sequence 66398, A					
Sequence 272863,					
Sequence 272863,					
Sequence 51, Appl					
Sequence 1814, Ap					
Sequence 10674, A					
Sequence 374, App					
Sequence 1997, Ap					
Sequence 471, App					
Sequence 43, Appl					

13	34.4	7.0	516	13	US-10-027-632-272862	Sequence 272862,
14	34.4	7.0	516	15	US-10-027-632-272862	Sequence 272862,
15	34.4	7.0	2000	16	US-10-260-238-2032	Sequence 2032, Ap
16	34.4	7.0	82293	16	US-10-433-580-1	Sequence 1, Appl
17	34.2	6.9	431	14	US-10-208-408-43	Sequence 43, Appl
18	34	6.9	7005	15	US-10-369-493-26248	Sequence 26248, A
19	33.8	6.9	481	16	US-10-240-425-1382	Sequence 1382, Ap
20	33.8	6.9	367378	15	US-10-312-841-2	Sequence 2, Appli
21	33.6	6.8	729	13	US-10-027-632-151539	Sequence 151539,
22	33.6	6.8	729	15	US-10-027-632-151539	Sequence 151539,
23	33.6	6.8	2000	16	US-10-260-238-1988	Sequence 1988, Ap
24	33.6	6.8	3493	13	US-10-027-632-112760	Sequence 112760,
25	33.6	6.8	3493	15	US-10-027-632-112760	Sequence 112760,
26	33.4	6.8	777	17	US-10-415-478A-35	Sequence 35, Appl
27	33.4	6.8	9223	8	US-08-961-527-59	Sequence 59, Appl
28	33.4	6.8	9223	16	US-10-158-844-59	Sequence 59, Appl
29	33.4	6.8	27540	17	US-10-415-478A-10	Sequence 10, Appl
30	33.2	6.7	139389	15	US-10-236-031B-61	Sequence 61, Appl
31	33	6.7	62909	16	US-10-672-787-32	Sequence 32, Appl
32	32.8	6.7	1324	16	US-10-424-599-121388	Sequence 121388,
33	32.8	6.7	5497	15	US-10-311-453-710	Sequence 710, App
34	32.8	6.7	13784	16	US-10-257-166-143	Sequence 143, App
35	32.8	6.7	21814	17	US-10-316-540-4	Sequence 4, Appli
36	32.6	6.6	364	16	US-10-424-599-93607	Sequence 93607, A
37	32.6	6.6	17142	14	US-10-239-676-206	Sequence 206, App
38	32.6	6.6	17142	15	US-10-311-455-2080	Sequence 2080, Ap
39	32.6	6.6	17142	15	US-10-240-453-304	Sequence 304, App
40	32.4	6.6	463	9	US-09-864-761-6488	Sequence 6488, Ap
41	32.4	6.6	478	13	US-10-027-632-186833	Sequence 186833,
42	32.4	6.6	478	15	US-10-027-632-186833	Sequence 186833,
43	32.4	6.6	1170	13	US-10-027-632-123172	Sequence 123172,
44	32.4	6.6	1170	15	US-10-027-632-123172	Sequence 123172,
45	32.4	6.6	1269	16	US-10-282-122A-40614	Sequence 40614, A

#### ALIGNMENTS

#### RESULT 1

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US-09-882-434A-2
; Sequence 2, Application US/09882434A
; Patent No. US20020108144A1
; GENERAL INFORMATION:
; APPLICANT: Manners, John M.
; APPLICANT: Marcus, John Paul
; APPLICANT: Goulter, Kenneth C.
; APPLICANT: Green, Jodie Lyn
; TITLE OF INVENTION: ANTI-MICROBIAL PROTEIN
; FILE REFERENCE: CULLN18.1CPI1
; CURRENT APPLICATION NUMBER: US/09/882,434A
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 09/364395
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: 09/117615
; PRIOR FILING DATE: 1998-11-09
; PRIOR APPLICATION NUMBER: PCT/AU97/00052
; PRIOR FILING DATE: 1997-01-31
; PRIOR APPLICATION NUMBER: AU PN 7802
; PRIOR FILING DATE: 1996-01-31
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; TYPE: DNA
; ORGANISM: Macadamia integrifolia
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (70)...(375)
; OTHER INFORMATION: y=t or c.
US-09-882-434A-2
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Query Match 99.9% Score 492.6; DB 9; Length 493;  
Best local Similarity 100.0%; Pred. No. 1e-140;

Matches 493; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 ATTAAGTCTTTGAGTCTCATACAPACTCTTCTCCCCACCATTAGCACTTATCAGCTA 60
Db 1 ATTAAGTCTTTGAGTCTCATACATACTCTTCTCCCCACCATTAGCACTTATCAGCTA 60
Qy 61 ACCTCAGCCATGGCTTCCACCAAGTGTCTTCTCAGTCATCTAGTATGATGCTCATA 120
Db 61 ACCTCAGCCATGGCTTCCACCAAGTGTCTTCTCAGTCATCTAGTATGATGCTCATA 120
Qy 121 GCAATGGCAAGTGAATGGTGAATGGAGTGCATTTACAGTATGGAGTGTCCAGGTTGT 180
Db 121 GCAATGGCAAGTGAATGGTGAATGGAGTGCATTTACAGTATGGAGTGTCCAGGTTGT 180
Qy 181 AACAACTGTGTGAGCGGATATAGCAAGTGTGGATGCTCAGCTATACATCAGAAGGAGGC 240
Db 181 AACAACTGTGTGAGCGGATATAGCAAGTGTGGATGCTCAGCTATACATCAGAAGGAGGC 240
Qy 241 TATGACTTCAGCTACACTGGAACAACTGCTCTCTACAACTGGAGTGTGGATGAGTGGT 300
Db 241 TATGACTTCAGCTACACTGGAACAACTGCTCTCTACAACTGGAGTGTGGATGAGTGGT 300
Qy 301 GTTGACACACACAGGTTTGGGTCCAGTCCAGGCGCATGCAACCCCTTTTGGTTGGAAGAGT 360
Db 301 GTTGACACACACAGGTTTGGGTCCAGTCCAGGCGCATGCAACCCCTTTTGGTTGGAAGAGT 360
Qy 361 ATCTTCATCCAAATGCTAGATTTCACTAATCTTGGATCCATCTTCTATGTTTTTCAAGTGT 420
Db 361 ATCTTCATCCAAATGCTAGATTTCACTAATCTTGGATCCATCTTCTATGTTTTTCAAGTGT 420
Qy 421 ATAATTAGAGAGATGCATGGATATATAATAAAGTAAAGTAAAGTAAAGTAAAGTAAAGT 480
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Qy 481 ATGATTTTAYACC 493
Db 481 ATGATTTTAYACC 493
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## RESULT 2

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US-10-425-115-66398/c
; Sequence 66398, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kowalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 66398
; LENGTH: 632
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(632)
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRF457_160554C.1
US-10-425-115-66398
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Query Match 8.0%; Score 39.6; DB 16; Length 632;
Best Local Similarity 55.7%; Pred. No. 0.22;
Matches 97; Conservative 0; Mismatches 74; Indels 3; Gaps 1;

Qy 203 GCAAGTGTGAGTCTCAGCTATACATCAGAGGGAGGCTATGACTTCTAGCTACACTGGAC 262
Db 394 GCTCGTGGCTGCAACCACTCCGTTTTCCAGGGGGCCAGAGTTCAACTTCCGGGGCG 335
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Qy 263 AAAGTGTCTCTCTACAAACAGGCTGGATGCTGTTGGACACACAGGTTTGGT 322
Db 334 AGAGGGCAAGCTCTACTCCAGCCGGCTGCTGGACGCCCTTACAGGTGTTCAGG 275
Qy 323 CCAGTGCAGGCGATGCAACCCCTTTTGGTTGGAAGAGTATCTTCATCCAATGCT 376
Db 274 ACA---CCAGGCTTGGCGGACTTCGGCTGGCAGATATCCACATCGACTGCT 224
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## RESULT 3

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US-10-027-632-272863
; Sequence 272863, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; POLYMORPHISMS IN THE HUMAN GENOME
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 272863
; LENGTH: 516
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-272863
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Query Match 7.2%; Score 35.6; DB 13; Length 516;
Best Local Similarity 50.6%; Pred. No. 3.3;
Matches 83; Conservative 1; Mismatches 80; Indels 0; Gaps 0;
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Qy 292 TGCAGTGTGTTCACACACACAGGTTTGGTCCAGTGCAGGCGCATGCAACCCCTTTGGT 351
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Qy 352 TGGAGAGTATCTTCATCCAATGCTAGATTTTCATAACTCTTGGATCCATCTTCTATGTTT 411
Db 378 TCAAGCCATAGCTCCATCAGTTACTAGATGTGTAACTTGGTGTATGAGCATCTATGTAC 437
Qy 412 TTCAAGTGTATAATTAGAGAGATGCATGATATATAATAATAA 455
Db 438 GTCAGTTTCATCAGTGAATGACAGTAAATAATAATACTGA 481
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## RESULT 4

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US-10-027-632-272863
; Sequence 272863, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; POLYMORPHISMS IN THE HUMAN GENOME
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
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; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 272863
; LENGTH: 516
; TYPE: DNA
; ORGANISM: Human
; US-10-027-632-272863

Query Match          7.2%; Score 35.6; DB 15; Length 516;
Best Local Similarity 50.6%; Pred. No. 3.3;
Matches 83; Conservative 1; Mismatches 80; Indels 0; Gaps 0;

.QY 292 TGCAGTGGTGTGCACACACAGGTTGGGTCCAGTCCAGGCGCATGCCAACCCTTTTGGT 351
Db 318 TTCAGATCAGTTGCAGCAAGAGTTAAGCATAGAGTCTCGGAGTTAGACTGCTGGGTC 377
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Db 378 TCAAGCATAGCTCCATCAGTTACTAGATGTGTAACCTTGGGTTATGAGCATCTAATGATC 437
QY 412 TTCAAGTGTATTAATTAGAGAGATGCATGGATATATAATAATAA 455
Db 438 GTCAGTTTCATCATGTAAGATGACAGTAATAATAATAACTGA 481

RESULT 5
US-10-311-455-51/c
; Sequence 51, Application US/10311455
; Publication No. US20030143606A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determ
; TITLE OF INVENTION: cytosine methylation
; FILE REFERENCE: 5013.1014
; CURRENT APPLICATION NUMBER: US/10/311,455
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: PCT/EP01/07537
; PRIOR FILING DATE: 2001-07-02
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 2424
; SEQ ID NO 51
; LENGTH: 8011
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-311-455-51

Query Match          7.2%; Score 35.6; DB 15; Length 8011;
Best Local Similarity 58.5%; Pred. No. 14;
Matches 62; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

QY 361 ATCTTCATCCAAATGCTAGATTTCAATCTTTGGATCCATCTTCTATGTTTTCAGAGTGT 420
Db 3147 ATCTAAATTTAACCAATCTACCTAAATCCAAACCATCTTTTAACTTTTCAATATA 3088
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QY 421 ATAAATTAGAGATGCGATGATATATAATAAATAAGTAAAGCTAC 466
Db 3087 TTACATAATTACATACAAACAAATAATAATAATAAAAAAACC 3042

RESULT 6
US-10-172-118-1814
; Sequence 1814, Application US/10172118
; Publication No. US20030224374A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Chris
; APPLICANT: Van 't Veer, Laura
; APPLICANT: Van de Vijver, Marc
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-175-999
; CURRENT APPLICATION NUMBER: US/10/172,118
; CURRENT FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 60/380,770
; PRIOR FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 1814
; LENGTH: 2035
; TYPE: DNA
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: NM_019049
; DATABASE ENTRY DATE: 2001-06-18
; US-10-172-118-1814

Query Match          7.2%; Score 35.4; DB 15; Length 2035;
Best Local Similarity 55.2%; Pred. No. 7.9;
Matches 69; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

QY 345 TTTTGGTTGGAAGAGTATCTTCATCCATGCGATGATTAATTAATAAGTAAAGCT 404
Db 1269 TATTGTAGGAATGGCAACTCATACTATTTAAATTTTTTTCGATTTCACATTTTC 1328
QY 405 TATGTTTTTCAAGTGATATAATTAGAGAGATGCGATGATATAATAATAAGTAAAGCT 464
Db 1329 TCACTTGTTTCATTTCCGAGGATATATGAATGATGATTTTAAATATAAGCGAATCT 1388
QY 465 ACGGT 469
Db 1389 ACTGT 1393

RESULT 7
US-10-342-887-1814
; Sequence 1814, Application US/10342887
; Publication No. US20040058340A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter S.
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Christopher J.
; APPLICANT: Van 't Veer, Laura Johanna
; APPLICANT: Van de Vijver, Marc J.
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-188-999
; CURRENT APPLICATION NUMBER: US/10/342,887
; CURRENT FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: 60/298,918
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 60/380,710
; PRIOR FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 10/172,118
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; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 1814
; LENGTH: 2035
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-342-887-1814

Query Match          7.2%; Score 35.4; DB 16; Length 2035;
Best Local Similarity 55.2%; Pred. No. 7.9;
Matches 69; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

QY 345 TTTTGGTTGAAGAGTATCTTCATCCAAATGCTAGATTTTCATACTCTTTGGATCCATCTTC 404
Db 1269 TATTTGAGAAATGGCAACTCACTACTATTAAATTTTTTTTGCATTGGCAACATTTTTC 1328

QY 405 TATGTTTTTCAAGTGTATAATTAGAGAGATGCGATGATATATAATAAATAAGTAAAAAGCT 464
Db 1329 TCACCTGTTCATTTCGAGGATATATGAATGCAATGTATTTTAAATATAAAGCGAATTC 1388

QY 465 ACGGT 469
Db 1389 ACTGT 1393

RESULT 8
US-10-198-846-10674
; Sequence 10674, Application US/10198846
; Publication No. US20030099974A1
; GENERAL INFORMATION:
; APPLICANT: Lillie, James
; APPLICANT: Xu, Yongyao
; APPLICANT: Wang, Youzhen
; APPLICANT: Steimann, Kathleen
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
; TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF BREAST CANCER
; FILE REFERENCE: MRI-049
; CURRENT APPLICATION NUMBER: US/10/198,846
; CURRENT FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/306,220
; PRIOR FILING DATE: 2001-07-18
; NUMBER OF SEQ ID NOS: 14084
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10674
; LENGTH: 2658
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 2641, 2642, 2643, 2644, 2645, 2646, 2647, 2648, 2649, 2650,
; LOCATION: 2651, 2652, 2653, 2654, 2655, 2656, 2657, 2658
; OTHER INFORMATION: n = A,T,C or G
US-10-198-846-10674

Query Match          7.2%; Score 35.4; DB 14; Length 2658;
Best Local Similarity 55.2%; Pred. No. 9.1;
Matches 69; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

QY 345 TTTTGGTTGAAGAGTATCTTCATCCAAATGCTAGATTTTCATACTCTTTGGATCCATCTTC 404
Db 1891 TATTTGAGAAATGGCAACTCACTACTATTAAATTTTTTTTGCATTGGCAACATTTTTC 1950

QY 405 TATGTTTTTCAAGTGTATAATTAGAGAGATGCGATGATATATAATAAATAAGTAAAAAGCT 464
Db 1951 TCACCTGTTCATTTCGAGGATATATGAATGCAATGTATTTTAAATATAAAGCGAATTC 2010

QY 465 ACGGT 469
Db 2011 ACTGT 2015

RESULT 9

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Db 2301 TTATATAAAATGTTTTTTTATTAGATAAATTTATTATAAATAATAGATTATTATAAGATA 2360

## RESULT 11

US-10-221-714A-471  
; Sequence 471, Application US/10221714A  
; Publication No. US20040048254A1  
; GENERAL INFORMATION:  
; APPLICANT: OLEK, Alexander  
; APPLICANT: PIEPENROCK, Christian  
; APPLICANT: BERLIN, Kurt  
; TITLE OF INVENTION: Diagnosis of Diseases Associated with  
; FILE REFERENCE: 5013.1005  
; CURRENT APPLICATION NUMBER: US/10/221,714A  
; CURRENT FILING DATE: 2003-01-21  
; PRIOR APPLICATION NUMBER: PCT/EP01/02955  
; PRIOR FILING DATE: 2001-03-15  
; PRIOR APPLICATION NUMBER: DE 10013847.0  
; PRIOR FILING DATE: 2000-03-15  
; PRIOR APPLICATION NUMBER: DE 10019058.8  
; PRIOR FILING DATE: 2000-04-06  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; PRIOR APPLICATION NUMBER: DE 10032529.7  
; PRIOR FILING DATE: 2000-06-30  
; PRIOR APPLICATION NUMBER: DE 10043826.1  
; PRIOR FILING DATE: 2000-09-01  
; NUMBER OF SEQ ID NOS: 540  
; SEQ ID NO 471  
; LENGTH: 38342  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)  
US-10-221-714A-471

Query Match 7.1%; Score 35.2; DB 16; Length 38342;  
Best Local Similarity 55.8%; Pred. No. 43;  
Matches 67; Conservative 0; Mismatches 53; Indels 0; Gaps 0;  
Qy 346 TTTCGGTGGAGAGATCTTCATCAATGCTAGATTTCATCACTCTTGGATCCATCTTCT 405  
Db 2241 TTTTTCGTAAGATTATTTTTTATTATGCGGGTTTTATTAGTTTTTTATTATGTTGA 2300  
Qy 406 ATGTTTTTCAAGTGTATATATTAGAGAGATGCATGATATATAATAAATAAGTAAAGCTA 465  
Db 2301 TTATATAAAATGTTTTTTTATTAGATAAATTTATTATAAATAATAGATTATTATAAGATA 2360

## RESULT 12

US-09-382-860-43/c  
; Sequence 43, Application US/09382860  
; Publication No. US20030110526A1  
; GENERAL INFORMATION:  
; APPLICANT: Brown, Jr., Robert H.  
; APPLICANT: Liu, Jing  
; APPLICANT: Aoki, Masashi  
; APPLICANT: Hoffman, Eric  
; APPLICANT: Chou, Fan-Li  
; TITLE OF INVENTION: DYSPERLIN MUTATIONS  
; FILE REFERENCE: 00786/401002  
; CURRENT APPLICATION NUMBER: US/09/382,860  
; CURRENT FILING DATE: 1999-08-25  
; EARLIER APPLICATION NUMBER: US 60/097,930  
; EARLIER FILING DATE: 1998-08-25  
; NUMBER OF SEQ ID NOS: 283  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 43  
; LENGTH: 179  
; TYPE: DNA  
; ORGANISM: Homo sapiens

## US-09-382-860-43

Query Match 7.1%; Score 34.8; DB 10; Length 179;  
Best Local Similarity 65.4%; Pred. No. 3.3;  
Matches 51; Conservative 0; Mismatches 27; Indels 0; Gaps 0;  
Qy 22 CATACTCTTCTCCCTCCACCATTTAGCACTTATCAGCTAACCTCAGGCATGGCTTCCACC 81  
Db 155 CCTGCTCCCTTGCTCTTACCATTTTCCCGCAAGCTGACCTCCACAAGGGGTCCACC 96  
Qy 82 AAGTTGTTCTTCTCAGTC 99  
Db 95 AAGTTCTTCTTGTTACTC 78

## RESULT 13

US-10-027-632-272862  
; Sequence 272862, Application US/10027632  
; Publication No. US20020198371A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
; FILE REFERENCE: 108827.129  
; CURRENT APPLICATION NUMBER: US/10/027,632  
; CURRENT FILING DATE: 2002-04-30  
; PRIOR APPLICATION NUMBER: US 60/218,006  
; PRIOR FILING DATE: 2000-07-12  
; PRIOR APPLICATION NUMBER: US 60/198,676  
; PRIOR FILING DATE: 2000-04-20  
; PRIOR APPLICATION NUMBER: US 60/193,483  
; PRIOR FILING DATE: 2000-03-29  
; PRIOR APPLICATION NUMBER: US 60/185,218  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/167,363  
; PRIOR FILING DATE: 1999-11-23  
; PRIOR APPLICATION NUMBER: US 60/156,358  
; PRIOR FILING DATE: 1999-09-28  
; PRIOR APPLICATION NUMBER: US 60/146,002  
; PRIOR FILING DATE: 1999-08-09  
; NUMBER OF SEQ ID NOS: 325720  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 272862  
; LENGTH: 516  
; TYPE: DNA  
; ORGANISM: Human  
US-10-027-632-272862

Query Match 7.0%; Score 34.4; DB 13; Length 516;  
Best Local Similarity 50.6%; Pred. No. 7.7;  
Matches 83; Conservative 0; Mismatches 81; Indels 0; Gaps 0;  
Qy 292 TGCAGTGGTGTTCACACACACAGGTTTGGGTCCAGTCCAGGCGCATGCAACCCCTTTGGT 351  
Db 318 TTCAGATCAGTTGCAGCAAGAGTTAAGATAAGAGTCTCTGGATTAGCTGCTGGGTC 377  
Qy 352 TGGAAAGATATCTTCATCCCAATGCTAGATTTCATACTCTTGGATCCATCTTCTATGTT 411  
Db 378 TCAAGCCATAGCTCCATCAGTTACTAGATGTGTAACCTTGGGTTATGAGCATCTATGTAC 437  
Qy 412 TTCAAGTGTATATAATTAGAGATCCATGGATATATAATAATAA 455  
Db 438 GTCAGTTCTTTCATCAGTGAATGACAGTAATAATAATACTGA 481

## RESULT 14

US-10-027-632-272862  
; Sequence 272862, Application US/10027632  
; Publication No. US20030204075A9  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
; FILE REFERENCE: 108827.129  
; CURRENT APPLICATION NUMBER: US/10/027,632  
; CURRENT FILING DATE: 2002-04-30  
; PRIOR APPLICATION NUMBER: US 60/218,006  
; PRIOR FILING DATE: 2000-07-12  
; PRIOR APPLICATION NUMBER: US 60/198,676  
; PRIOR FILING DATE: 2000-04-20  
; PRIOR APPLICATION NUMBER: US 60/193,483  
; PRIOR FILING DATE: 2000-03-29  
; PRIOR APPLICATION NUMBER: US 60/185,218  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/167,363  
; PRIOR FILING DATE: 1999-11-23  
; PRIOR APPLICATION NUMBER: US 60/156,358  
; PRIOR FILING DATE: 1999-09-28  
; PRIOR APPLICATION NUMBER: US 60/146,002  
; PRIOR FILING DATE: 1999-08-09  
; NUMBER OF SEQ ID NOS: 325720  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 272862  
; LENGTH: 516  
; TYPE: DNA  
; ORGANISM: Human  
US-10-027-632-272862

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FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 272862
LENGTH: 516
TYPE: DNA
ORGANISM: Human
US-10-027-632-272862
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Query Match 7.0%; Score 34.4; DB 15; Length 516;
Best Local Similarity 50.6%; Pred. No. 7.7;
Matches 83; Conservative 0; Mismatches 81; Indels 0; Gaps 0;

QY 292 TGCAGTGGTGTGGACACACAGAGTTTGGGTCCAGTGCAGGGCATGCAACCCCTTTGGT 351
DB 318 TTCAGATCAGTTCGCGAAGAGTTAAGCTAGAGTCTTGGAGTTAGACTGCTGGGTC 377

QY 352 TGGAGAGTATCTTCATCCAAATGCTAGATTTCATTAACCTCTTGGATCCATCTTCTATGTTT 411
DB 378 TCAAGCCATAGTCCCATCAGTTACTAGATGTGTACCTTTGGTTATGAGCATCTATGTAC 437

QY 412 TTCAAGTGTATAATTAGAGAGATGCATGCGATATATAATAATAA 455
DB 438 GTCAGTTTCTTCATCAGTGAATGACAGTAATAATAAATACTGA 481
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RESULT 15
US-10-260-238-2032/c
Sequence 2032, Application US/10260238
Publication No. US20040016025A1
GENERAL INFORMATION:
APPLICANT: Budworth, Paul R.
APPLICANT: Moughamer, Todd G.
APPLICANT: Briggs, Steven P.
APPLICANT: Cooper, Bret
APPLICANT: Glazebrook, Jane
APPLICANT: Goff, Stephen A.
APPLICANT: Katagiri, Fumiaki
APPLICANT: Kreps, Joel
APPLICANT: Provart, Nicholas
APPLICANT: Ricke, Darrell
APPLICANT: Zhu, Tong
TITLE OF INVENTION: PROMOTERS FOR REGULATION OF PLANT EXPRESSION
FILE REFERENCE: 60111-NP
CURRENT APPLICATION NUMBER: US/10/260,238
CURRENT FILING DATE: 2002-09-26
PRIOR APPLICATION NUMBER: US 60/325,448
PRIOR FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: US 60/325,277
PRIOR FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: US 60/370,620
PRIOR FILING DATE: 2002-04-04
NUMBER OF SEQ ID NOS: 6077
SEQ ID NO 2032
LENGTH: 2000
TYPE: DNA
ORGANISM: Oryza sativa
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US-10-260-238-2032
Query Match 7.0%; Score 34.4; DB 16; Length 2000;
Best Local Similarity 65.8%; Pred. No. 16;
Matches 50; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 390 CTTGGATCCATCTTCTATGTCTTCAAGTGTATATTAATTAGAGAGATGCATGATATATAAT 449
DB 1389 CTTAATTTCACTACAAATGTTTCCATTAGAGATTAAGAAATGCTTGGATGGATCAT 1330

QY 450 AAATAAGTAAAGCTA 465
DB 1329 CAATCAATAATAACCA 1314
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Search completed: November 5, 2004, 21:55:39
Job time : 382 secs
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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 5, 2004, 21:49:14 ; Search time 102 Seconds  
(without alignments)  
353.226 Million cell updates/sec

Title: US-09-882-434A-1

Perfect score: 551

Sequence: 1 MASTKLFSSVITVWMLIAMA.....FGSSARACNPFQWKSIFIQC 102

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1566620 seqs, 353225886 residues

Total number of hits satisfying chosen parameters: 1566620

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*

- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*
- 5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*
- 6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep.\*
- 7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep.\*
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- 9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pep.\*
- 10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep.\*
- 11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep.\*
- 12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep.\*
- 13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*
- 14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*
- 15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep.\*
- 16: /cgn2\_6/ptodata/1/pubpaa/US10D\_PUBCOMB.pep.\*
- 17: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.\*
- 18: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep.\*
- 19: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*
- 20: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	551	100.0	102	9	US-09-882-434A-1
2	426	77.3	76	9	US-09-882-434A-15
3	426	77.3	76	9	US-09-882-434A-16
4	426	77.3	76	9	US-09-882-434A-17
5	421	76.4	76	9	US-09-882-434A-18
6	419	76.0	76	9	US-09-882-434A-19
7	417	75.7	76	9	US-09-882-434A-21
8	415	75.3	76	9	US-09-882-434A-20
9	183	33.2	116	17	US-10-425-115-251061
10	80.5	14.6	500	15	US-10-424-599-214772
11	75.5	13.7	486	9	US-09-801-368-154
12	75.5	13.7	486	14	US-10-369-493-21896
13	73.5	13.3	232	15	US-10-424-599-179163

14	73	13.2	92	16	US-10-437-963-184834	Sequence 184834, A
15	72	13.1	507	14	US-10-156-761-10129	Sequence 10129, A
16	71.5	13.0	403	15	US-10-282-122A-55057	Sequence 55057, A
17	71	12.9	68	17	US-10-425-115-303206	Sequence 303206, A
18	71	12.9	235	17	US-10-739-930-10191	Sequence 10191, A
19	71	12.9	1280	14	US-10-101-433A-3	Sequence 3, Appli
20	71	12.9	1280	15	US-10-619-359A-2	Sequence 2, Appli
21	71	12.9	1283	14	US-10-101-433A-2	Sequence 2, Appli
22	71	12.9	1283	14	US-10-101-433A-4	Sequence 4, Appli
23	71	12.8	1283	15	US-10-619-359A-4	Sequence 4, Appli
24	70.5	12.8	267	9	US-09-764-868-1164	Sequence 1164, Ap
25	70.5	12.8	267	10	US-09-764-891-4089	Sequence 4089, Ap
26	70	12.7	167	16	US-10-437-963-151301	Sequence 151301, A
27	69	12.5	1280	13	US-10-044-671-2	Sequence 2, Appli
28	69	12.5	1280	14	US-10-101-433A-11	Sequence 11, Appli
29	69	12.5	1280	15	US-10-619-359A-7	Sequence 7, Appli
30	69	12.5	1281	14	US-10-101-433A-7	Sequence 7, Appli
31	69	12.5	1281	14	US-10-101-433A-8	Sequence 8, Appli
32	69	12.5	1281	14	US-10-101-433A-9	Sequence 9, Appli
33	68.5	12.4	78	14	US-10-101-433A-10	Sequence 10, Appl
34	68.5	12.4	1557	14	US-10-178-213-431	Sequence 431, App
35	68.5	12.4	1887	10	US-09-369-493-6816	Sequence 6816, Ap
36	68.5	12.4	174	15	US-10-424-599-253845	Sequence 253845, A
37	68	12.3	461	14	US-10-081-872-82	Sequence 82, Appl
38	68	12.3	461	14	US-10-105-733-10	Sequence 10, Appl
39	68	12.3	461	14	US-10-081-739A-10	Sequence 10, Appl
40	68	12.3	461	15	US-10-385-305-82	Sequence 82, Appl
41	68	12.3	579	9	US-09-805-020-67	Sequence 67, Appl
42	68	12.3	1278	9	US-09-805-020-66	Sequence 66, Appl
43	68	12.3	1280	9	US-09-817-762-3	Sequence 3, Appli
44	68	12.3	1280	9	US-09-866-866A-2	Sequence 2, Appli

## ALIGNMENTS

### RESULT 1

US-09-882-434A-1  
; Sequence 1, Application US/09882434A  
; Patent No. US20020108144A1  
; GENERAL INFORMATION:  
; APPLICANT: Manners, John M.  
; APPLICANT: Marcus, John Paul  
; APPLICANT: Goulter, Kenneth C.  
; APPLICANT: Green, Jodie Lyn  
; TITLE OF INVENTION: ANTI-MICROBIAL PROTEIN  
; FILE REFERENCE: CULN18.1CPI1  
; CURRENT FILING DATE: 2001-06-15  
; PRIOR FILING DATE: 1999-07-30  
; PRIOR FILING DATE: 1999-07-30  
; PRIOR FILING DATE: 1998-11-09  
; PRIOR FILING DATE: 1997-01-31  
; PRIOR FILING DATE: 1997-01-31  
; PRIOR FILING DATE: 1996-01-31  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 102  
; TYPE: PRT  
; ORGANISM: Macadamia integrifolia  
US-09-882-434A-1

Query Match 100.0%; Score 551; DB 9; Length 102;  
Best Local Similarity 100.0%; Pred. No. 7.5e-56;  
Matches 102; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASTKLFSSVITVWMLIAMASEMVNGSAFTVWSPGNCNNRAERYSKGCSAIHQKGYDF 60  
DB 1 MASTKLFSSVITVWMLIAMASEMVNGSAFTVWSPGNCNNRAERYSKGCSAIHQKGYDF 60



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; Sequence 19, Application US/09882434A
; Patent No. US20020108144A1
; GENERAL INFORMATION:
; APPLICANT: Manners, John M.
; APPLICANT: Marcus, John Paul
; APPLICANT: Goulter, Kenneth C.
; APPLICANT: Green, Jodie Lyn
; TITLE OF INVENTION: ANTI-MICROBIAL PROTEIN
; FILE REFERENCE: CULLN18.1CPI1
; CURRENT APPLICATION NUMBER: US/09/882.434A
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 09/364395
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: 09/117615
; PRIOR FILING DATE: 1998-11-09
; PRIOR APPLICATION NUMBER: PCT/AU97/00052
; PRIOR FILING DATE: 1997-01-31
; PRIOR APPLICATION NUMBER: AU PN 7802
; PRIOR FILING DATE: 1997-01-31
; PRIOR APPLICATION NUMBER: 09-882-434A-19
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 76
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: M154K variant. Variant MiAMP1 protein M154K
; OTHER INFORMATION: containing a Lysine at amino acid 54 (used primer
; OTHER INFORMATION: from SEQ ID NO:12 to produce).
; US-09-882-434A-19

Query Match 76.4%; Score 421; DB 9; Length 76;
Best Local Similarity 98.7%; Pred. No. 6.1e-41;
Matches 75; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 27 SAFTVWSGPGCNNAERYSKGCSAIHQKGYDFSITGQTAALYNQAGCSGVVHTRFGSS 86
Db 1 SAFTVWSGPGCNNAERYSKGCSAIHQKGYDFSITGQTAALYNQAGCSGVVHTRFGSS 60

Qy 87 ARACNPFGWKSIFIQ 102
Db 61 ARACNPFGWKSIFIQ 76

RESULT 6
US-09-882-434A-18
; Sequence 18, Application US/09882434A
; Patent No. US20020108144A1
; GENERAL INFORMATION:
; APPLICANT: Manners, John M.
; APPLICANT: Marcus, John Paul
; APPLICANT: Goulter, Kenneth C.
; APPLICANT: Green, Jodie Lyn
; TITLE OF INVENTION: ANTI-MICROBIAL PROTEIN
; FILE REFERENCE: CULLN18.1CPI1
; CURRENT APPLICATION NUMBER: US/09/882.434A
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 09/364395
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: 09/117615
; PRIOR FILING DATE: 1998-11-09
; PRIOR APPLICATION NUMBER: PCT/AU97/00052
; PRIOR FILING DATE: 1997-01-31
; PRIOR APPLICATION NUMBER: AU PN 7802
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 76
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: M154V variant. Variant MiAMP1 protein M154V
; OTHER INFORMATION: containing a Lysine at amino acid 54 (used primer
; OTHER INFORMATION: from SEQ ID NO:11 to produce).
; US-09-882-434A-18

Query Match 75.0%; Score 419; DB 9; Length 76;
Best Local Similarity 98.7%; Pred. No. 1e-40;
Matches 75; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 27 SAFTVWSGPGCNNAERYSKGCSAIHQKGYDFSITGQTAALYNQAGCSGVVHTRFGSS 86
Db 1 SAFTVWSGPGCNNAERYSKGCSAIHQKGYDFSITGQTAALYNQAGCSGVVHTRFGSS 60

Qy 87 ARACNPFGWKSIFIQ 102
Db 61 ARACNPFGWKSIFIQ 76

RESULT 7
US-09-882-434A-21
; Sequence 21, Application US/09882434A
; Patent No. US20020108144A1
; GENERAL INFORMATION:
; APPLICANT: Manners, John M.
; APPLICANT: Marcus, John Paul
; APPLICANT: Goulter, Kenneth C.
; APPLICANT: Green, Jodie Lyn
; TITLE OF INVENTION: ANTI-MICROBIAL PROTEIN
; FILE REFERENCE: CULLN18.1CPI1
; CURRENT APPLICATION NUMBER: US/09/882.434A
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 09/364395
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: 09/117615
; PRIOR FILING DATE: 1998-11-09
; PRIOR APPLICATION NUMBER: PCT/AU97/00052
; PRIOR FILING DATE: 1997-01-31
; PRIOR APPLICATION NUMBER: AU PN 7802
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 76
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: M146K/54K variant. Variant MiAMP1 protein
; OTHER INFORMATION: M146K/54K containing a Lysine at amino acid 46 and
; OTHER INFORMATION: a Lysine at amino acid 54.
; US-09-882-434A-21

Query Match 75.7%; Score 417; DB 9; Length 76;
Best Local Similarity 97.4%; Pred. No. 1.8e-40;
Matches 74; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 27 SAFTVWSGPGCNNAERYSKGCSAIHQKGYDFSITGQTAALYNQAGCSGVVHTRFGSS 86
Db 1 SAFTVWSGPGCNNAERYSKGCSAIHQKGYDFSITGQTAALYNQAGCSGVVHTRFGSS 60

Qy 87 ARACNPFGWKSIFIQ 102
Db 61 ARACNPFGWKSIFIQ 76

RESULT 8
US-09-882-434A-20
; Sequence 20, Application US/09882434A
; Patent No. US20020108144A1
; GENERAL INFORMATION:
; APPLICANT: Manners, John M.
; APPLICANT: Marcus, John Paul
; APPLICANT: Goulter, Kenneth C.
; APPLICANT: Green, Jodie Lyn
; TITLE OF INVENTION: ANTI-MICROBIAL PROTEIN
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; FILE REFERENCE: CULLN18.1CPI1
; CURRENT APPLICATION NUMBER: US/09/882.434A
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 09/364395
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: 09/117615
; PRIOR FILING DATE: 1998-11-09
; PRIOR APPLICATION NUMBER: PCT/AU97/00052
; PRIOR FILING DATE: 1997-01-31
; PRIOR APPLICATION NUMBER: AU PN 7802
; PRIOR FILING DATE: 1996-01-31
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 76
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: M146K/54V variant. Variant MiAMP1 protein
; OTHER INFORMATION: M146K/54V containing a Lysine at amino acid 46 and
; OTHER INFORMATION: a Valine at amino acid 54.
US-09-882-434A-20

Query Match 75.3%; Score 415; DB 9; Length 76;
Best Local Similarity 97.4%; Pred. No. 3e-40; 1; Indels 0; Gaps 0;
Matches 74; Conservative 1; Mismatches 1;

QY 27 SAFTWSPGNCNRAERYSKGCSAIHOKGGYDFSYTGQTAALYNQAGCSGVVHTRFGSS 86
Db 1 SAFTWSPGNCNRAERYSKGCSAIHOKGGYDFSYTGQTAALYNKAGCSGVVHTRFGSS 60

QY 87 ARACNPPGKWSIFIQC 102
Db 61 ARACNPPGKWSIFIQC 76

RESULT 9
US-10-425-115-251061
; Sequence 251061, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 251061
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_160554C.1.pep
US-10-425-115-251061

Query Match 33.2%; Score 183; DB 17; Length 116;
Best Local Similarity 36.1%; Pred. No. 3.5e-13;
Matches 43; Conservative 17; Mismatches 39; Indels 20; Gaps 5;

QY 1 MASTK---LFFSVITVMMLIA-----MASEMVNGSAFTVWSPGNCNRAERY--- 44
Db 1 MASTKAATMF--VATAVVAIAATVAAATGWASDCSPSYLTWSGPGGCTTGKGHAS 58

QY 45 -SKGCSAIHOKGYDFSYTGQTAALYNQAGCSGVVHTRFGSSARACNPPGKWSIFIQC 102
Db 59 AGSCGCNHLRFHGHGFNFRGTATLYSQPCVGTPIQVF-EDTQACGDFGWSIHIDC 116

RESULT 10
US-10-424-599-214772
; Sequence 214772, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 214772
; LENGTH: 500
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(500)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_35966C.1.pep
US-10-424-599-214772

Query Match 14.6%; Score 80.5; DB 15; Length 500;
Best Local Similarity 29.3%; Pred. No. 1.3; 19; Indels 31; Gaps 7;
Matches 24; Conservative 8; Mismatches 19;

QY 34 GPGCNCNRAERYSKGCSAIHOKGG-----YDFSYTGQTAALYNQAGCS-----GVAHTR 82
Db 145 GSGCEG-----GCRVVHASNGVRRSAVEFGH-----LHSHA-CSCFGVXGIGKSKR 189

QY 83 FGSSARACNPPGKWSIFIQC 102
Db 190 FG---KICKPLTWKHGDIPLMC 208

RESULT 11
US-09-801-368-154
; Sequence 154, Application US/09801368
; Patent No. US20020128250A1
; GENERAL INFORMATION:
; APPLICANT: Busby, Robert
; APPLICANT: Cali, Brian
; APPLICANT: Hecht, Peter
; APPLICANT: Holtzman, Doug
; APPLICANT: Madden, Kevin
; APPLICANT: Maxon, Mary
; APPLICANT: Milne, Todd
; APPLICANT: No. US20020128250A1man, Thea
; APPLICANT: Royer, John
; APPLICANT: Salama, Sofie
; APPLICANT: Sherman, Amir
; APPLICANT: Silva, Jeff
; APPLICANT: Summers, Eric
; TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
; FILE REFERENCE: 109272.147
; CURRENT APPLICATION NUMBER: US/09/801,368
; CURRENT FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: US 09/487,558
; PRIOR FILING DATE: 2000-01-19
; PRIOR APPLICATION NUMBER: US 60/160,587
; PRIOR FILING DATE: 1999-10-20
; NUMBER OF SEQ ID NOS: 440
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 154
; LENGTH: 486
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-09-801-368-154
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Query Match          13.3%; Score 73.5; DB 15; Length 232;  
Best Local Similarity 22.3%; Pred. No. 3.;  
Matches 27; Conservative 14; Mismatches 27; Indels 53; Gaps 5;  
  
Qy      8 FSVITVMMILAMAS-----EMVNGSAFTW--SGPCNNRABRYSKGC 49  
       :|::||::|::|::|::|::|::|::|::|:  
Db     2 YLSISQMVLALCSLTTLAPLATIHAANFEIYVNCPYTVAASPGGGRLDR-----55  
       ||::|::|::|::|::|::|::|::|:  
Qy    50 SAHQKGGYDFSVTGOT-----AALYNQAGC---SGVAHPRFGSSARACNPF 94  
       |::|::|::|::|::|::|::|::|:  
Db   56 -----GQTWNLVNPGTATARIWGRTCTCFDPSGRRCQTDGCTGGLNCQG 101  
       |||||  
  
Qy    95 W 95  
       |  
Db   102 W 102  
  
RESULT 14  
US-10-437-963-184834  
 ; Sequence 184834, Application US/10437963  
 ; Publication No. US20040123343A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: La Rosa, Thomas J.  
 ; APPLICANT: Kovalic, David K.  
 ; APPLICANT: Zhou, Yihua  
 ; APPLICANT: Cao, Yongwei  
 ; APPLICANT: Wu, Wei  
 ; APPLICANT: Boukharov, Andrey A.  
 ; APPLICANT: Barbazuk, Brad  
 ; APPLICANT: Li, Ping  
 ; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With Plant Growth Promotion  
 ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
 ; FILE REFERENCE: 38-21(53221)B  
 ; CURRENT APPLICATION NUMBER: US/10/437,963  
 ; CURRENT FILING DATE: 2003-05-14  
 ; NUMBER OF SEQ ID NOS: 204966  
 ; SEQ ID NO 184834  
 ; LENGTH: 92  
 ; TYPE: PRT  
 ; ORGANISM: Oryza sativa  
 ; FEATURE:  
 ; OTHER INFORMATION: Clone ID: PAT_MRT4530_8178C.1.pep  
US-10-437-963-184834
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Query Match          13.2%; Score 73; DB 16; Length 92;  
Best Local Similarity 32.8%; Pred. No. 1.5;  
Matches 21; Conservative 5; Mismatches 16; Indels 22; Gaps 3;  
  
Qy    31 VWGSF-PGCCNR---AERYSKCCSIAHKQGYDFSYTGTTAAALYNQAAGCGVAHTRF 84  
       |||||  
Db   19 VWSGSTPVCNSGVHVVEDAAAACHGAHRFRFD-----ACTIHRRGF 62  
       |||||
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Db      19 VMSGSRTPVCSNWHVVVEDAAACGCHGAHRRFGRD-----AGTIIHRGFG 62
Qy      85 SSAR 88
Dd      ||
        63 HDAR 66

RESULT 15
US-10-156-761-10129
; Sequence 10129, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIOYUKI
; APPLICANT: HATTORI, MASAHERA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29

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; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 10129
; LENGTH: 507
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-10129

Query Match      13.1%; Score 72; DB 14; Length 507;
Best Local Similarity 24.3%; Pred. No. 13;
Matches 25; Conservative 19; Mismatches 43; Indels 16; Gaps 3;

Qy      1 MASTKLFPSVITVWML-----IASEMVMNGSAFTVWSGPGCN-NRAERYSKGCSAIH 53
Db      390 IVQSEIFGPVLVLPFDSDDEGIRLANDTPYGLAASAMSRDVIYRANRATREIKAGCYWVN 449
Qy      54 Q-----KGYDFSVYTGQTALYNOAGCGVAHTRFGSSA 87
Db      450 DHIPIISEMPHGGYKASGFGKMSAYSFEYTKIKHVMFDNTA 492

Search completed: November 5, 2004, 22:04:53
Job time : 104 secs
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